Supplemental material:

Supplemental Methods

Search strategy and selection criteria; Genetic studies

Reference lists of articles identified from the primary search were additionally scanned for relevant articles, including previous meta-analyses and systematic reviews. For inclusion, genetic studies had to have more than 500 participants, involve unrelated subjects and be published as full length articles or letters in a peer reviewed journal. Authors of published studies were contacted (on at least 3 occasions) to obtain additional information on *CETP* genotypes and variables of interest, where unreported. The collaborative group for the genetic analysis was assembled by direct contact with principal investigators of any study known to the authors that involved more than 500 individuals that had previously reported at least one genetic finding, in any area, in a peer reviewed journal.

Twenty two studies were identified from the search and the published meta-analysis and seven were either reported after the previously published meta-analysis, or were contacted independently of the search as these studies were known to have published on genetic associations in lipids. Where data were duplicated in two publications, clarity was sought from the author, and limited tabular data were requested on the complete cohort. If there was no response, the larger of the data sets reported were included. Four unpublished cohorts were included.

Data Extraction

Randomised trials: Information was extracted on treatment regimen and comparator, pre- and post-treatment concentration of HDL-, LDL- and total cholesterol, triglycerides, apolipoproteins A-I (apoA-I) apolipoprotein B (apo-B), C-reactive protein (CRP), sodium, potassium, chloride, and bicarbonate, aldosterone, plasma creatinine and estimated glomerular filtration rate, systolic and diastolic blood pressure.

Genetic Studies: Information was obtained on study design, total number of participants and the number of individuals by genotype category, gender, ethnic origin and presence or absence of CHD at baseline. In addition, summary information on the following variables was obtained (where available) for each *CETP*-genotype group: CETP concentration, CETP activity, HDL-, LDL-, and total cholesterol, triglycerides, apoA-I and apoA-II, apoB, HDL sub-fractions 2 and 3, systolic and diastolic blood pressure, blood glucose, CRP, urinary and plasma sodium, potassium and creatinine, body mass index, smoking status, age and treatment with anti-hypertensive medications or statins.

Statistical Analysis

For continuous traits, median values were assumed to be equal to mean values. If the standard deviation (SD) was not reported this was calculated from the standard error (SE) by multiplying the this by the square root of the sample size or from the inter-quartile range by dividing the width of the inter-quartile range by 1.349. For dose ranging studies, the SD was imputed from the largest study if unavailable. Where logged values were provided, these were back transformed and geometric means were used as means. Where cholesterol and triglycerides were reported in mg/ dl, values were converted to mmol/l by multiplying by 0.02586 and 0.01129 respectively. Similarly where glucose was reported as mg/dl values were converted to mmol/l by multiplying by 0.055, and creatinine was converted to µmol/L by multiplying by 88. We estimated using a MAF of 0.48, a sample size of 14,147 individuals was required to be able to detect a difference of 0.5 mmHg SBP, with a power of 0.8 at a significance of 0.05 (calculated using online genetic power calculator "Quanto" (S40)).

Simulation of observed gene vs expected torcetrapib dose equivalent effects: Once a linear dose response was confirmed for available variables, the summary effect with most data from dose finding or randomized trials (60mg) on HDL-C was used for simulation studies. The effect of 60 mg torcetrapib on HDL was called βd1(with standard error sd1), and for other i traits, similarly β_{di}(with standard error s_{di}). The simulation model then incorporated the variance in the effect estimates of the genotype and drug effects. This was done as follows: Firstly, a random draw (x_{d1}) of the 60mg drug effect on HDL cholesterol was taken from a normal distribution N($\beta_{d1,}s_{d1}$) and of the effect on each other trait (random draw x_{di} from N(β_{di},s_{di}), and of the gene effect on HDL cholesterol (draw x_{g1} from N($\beta_{g1,}s_{g1}$). The gene effect (x_{g1}) was then expressed as a torcetrapib dose equivalent, calculated as $dose_g=60\ x_{g1}/x_{d1}$, from which the expected effect of this dose on trait *i* was estimated as $e_{gi}=x_{di}x_{g1}/x_{d1}$,. Random draws were repeated 100000 times, generating a distribution of $dose_g$ from which its mean, 2.5^{th} and 97.5^{th} percentiles were used to estimate the mean (95% confidence interval) for the gene-dose equivalent. Similarly the mean of the distribution of expected effects on trait *i* was estimated (m_e_{gi}) as well as its standard error (s_{egi}) as (97.5^{th}-2.5^{th} percentiles)/(2x1.96). The observed gene effect on trait i (β_{gi}) was compared to the expected effect of a comparable dose of torcetrapib (m_e_{gi}) using a Z- test, $z=(\beta_{gi}-m\_e_{gi})/\sqrt{(s_{gi}^2+ s_{egi}^2)}$.

Consistency between the CETP gene effects and equivalent torcetrapib dose

The 95% confidence intervals for the expected effect of a dose of torcetrapib comparable to the effect of genotype were obtained by simulation. To incorporate the uncertainty in the effect estimates, one hundred thousand replications were generated of the point estimates and standard errors of the 60 mg dose of torcetrapib. The values of the 2.5 and 97.5 centiles of the simulated distribution were uses as the 95% confidence intervals. The simulation process was conducted separately for individuals homozygous for the B2 allele and then repeated for heterozygous individuals.

Supplemental Results

Seven studies with 21, 353 individuals homozygous for the rs5882 (I405V) allele also had higher concentrations of HDL cholesterol (0.04 mmol/L; 0.00, 0.09), although the effect is less marked than that of rs7082872 (Taq1B). Similarly there was no evidence of a link between the I405V variant and blood pressure.

Supplemental Tables:

Table S1: Effect of torcetrapib (60 mg) and *CETP* genotype on other continuous and demographic variables.

Differences between continuous traits are those reported at the end of the randomised trial end unless otherwise indicated. Differences in demographic variables for RCTs were those recorded at baseline. ** only ILLUMINATE contributed to analysis.

Comparison	RCTs, Torcetrapib 60 mg (Number of Individuals)	Summary Mean Difference/ Odds Ratio (95% CI)	P value	Genetic Studies, B1B2 vs B1B1, no of studies (Individuals)	Summary Mean Difference/ Odds Ratio (95%CI)	P Value	Genetic Studies, B2B2 vs B1B1, no of studies (Individuals)	Summary Mean Difference/ Odds Ratio (95%CI)	P Value
Continuous traits									
C-reactive protein (mg/L)	2 (17,007)	0.02 (-0.04, 0.08)	0.52	13 (34,826)	0.03 (-0.07, 0.13)	0.60	13 (22,049)	0.16 (0.04, 0.29)	0.01
Glucose (mmol/L)	NA	NA	NA	11 (32,608)	0.00 (-0.02, 0.02)	0.95	11 (20,497)	0.03 (0.00, 0.06)	0.09
Demographic amd other variables									
Age	4 (17,911)	-0.48 (-1.29, 0.33)	0.25	19 (43,950)	0.00 (-0.20, 0.21)	0.98	19 (27,583)	0.18 (0.00, 0.35)	0.05
BMI (kg/m^2)	4 (17,911)	-0.06 (-0.22, 0.1)	0.46	19 (40,212)	-0.07 (0.15, 0.02)	0.12	19 (25,249)	-0.01 (-0.12, 0.10)	0.85
Treatment with statin	4 (17,911)	All treated with Atorvastatin	All treated with Atorvastatin	7 (20,600)	1.02 (0.10, 10.74)	0.99	7 (13,005)	0.92 (0.09, 9.79)	0.95
Treatment anti-hypertensive medication	3 (2,844)	0.98 (0.07, 13.3)	0.99	7 (20,077)	0.99 (0.83,1.17)	0.87	10 (15,154)	0.98 (0.80, 1.21)	0.85
Hypertension at baseline	4 (17,911)	1.04 (0.05, 22.5)	0.99	NA	NA	NA	NA	NA	NA
Current/ former vs never smoked	NA	NA	NA	9 (23,420)	0.92 (0.82, 1.03)	0.16	9 (14,649)	0.90 (0.78,1.04)	0.15

Table S2. Studies contributing to the CETP analysis

Study	Year of publication	Country	Gender male (%)	Mean age (years)	Total sample (n)	Study Description	Baseline coronary heart disease (CHD)	HWE χ^2 for main genotype included	CETP SNP(s) typed
*Published studies with blood pressure, **studies that did not respond to data request									
REGRESS[S30*]	1998	Netherlands	100	56	807	Cases of CHD from RCT	CHD	0.33	rs708272
Corella D [S11**]	1999	Spain	45	36.6	514	Cross sectional	No CHD	1.18	rs708272
Rekyavik [S13**]	2000	Iceland	100	71	1,134	Prospective cohort study - cases of CHD only	CHD	4.45	rs708272
Brousseau M [S9**]	2002	United States	100	64	833	Cross Sectional	CHD	3.71	rs708272
Atherogene [S6**]	2003	Germany	75	64.4	1,211	Prospective cohort of CHD	CHD	1.98	rs1800775
CARE[S12*]	2004	Canada, United States	86	59.5	3,205	Cases from RCT	CHD	1.78	rs708272
PHS [S24 **]	2005	United States	100	58.4	768	Prospective cohort	Mixed Population	1.01	rs708272
Marschang P [S31**]	2006	Austria	56	64.3	983	Prospective Cohort	CHD	0.06	rs708272
⁺Studies with unpublished data on blood pressure, ⁺unpubublished studies									
EARS[S16+]	1999	Estonia, Belgium, Denmark, Finland, Germany, Greece, Italy, Portugal, Spain, Switzerland, United Kingdom	100	23	794	Cross sectional	No CHD	0.00	rs708272, rs5882
OPERA[S18,S19,S20+]	2000	Finland	49	51.4	524	Prospective cohort	Mixed Population	0.02	rs708272, rs158477
Framingham Offspring[S29+]	2000	United States	48.4	51.3	2,916	Prospective cohort	Mixed Population	1.84	rs708272
Arca M[S4+]	2001	Italy	65.4	58.7	798	Case control, additional group of population controls	Mixed Population	0.88	rs708272
ECTIM[S10,S15,S22+]	2002	France, United Kingdom	78	55.5	2,540	Case control	Mixed Population	1.27	rs708272, rs5882, rs1800775, G-971A
NPHS[S26+]	2002	United Kingdom	100	55.9	2,589	Prospective Cohort	No CHD	3.4	rs708272
WOSCOPS[S14+]	2003	United Kingdom	100	57	1,604	RCT	Mixed Population	0.28	rs708272
ACCESS[S25+]	2005	United states	60	60.3	2,106	RCT	Mixed Population	0.01	72 SNPs incuding rs708282, rs5882, rs1800775
Sorli[S27+]	2006	Spain	31	45.5	549	Cross sectional	Mixed Population	0.99	rs708272
PREVEND[S8+]	2006	Netherlands	50.5	49.4	8,166	Prospective cohort	Mixed Population	1.56	rs708272, rs1800775, rs5882
SAPHIR[S28+]	2008	Austria	68	52.7	1,503	Prospective Cohort	No CHD	0.31	rs708272
Busselton[S1+]	2007	Australia	45	49	1,574	Cross sectional	Mixed Population	1.05	rs708272, rs1800775, rs12149545
CUDAS[S1+]	2007	Australia	50	53	1,109	Cross sectional	Mixed Population	0.01	rs708272, rs1800775, rs12149546
CUPID[S1+]	2007	Australia	87	50	556	Cohort of patients presenting for coronary catheters	CHD	0.12	rs708272, rs1800775, rs12149547
Intermountain[S17+]	2007	United States	69	56	9,371	Cohort of patients presenting for coronary catheters	Mixed Population	1.22	32 SNPs incuding rs708282, rs5882, rs1800775
Health Professionals Study[S23+]	2007	United States	100	60	2,193	Prospective cohort study	No CHD	0.945	rs708272
Nurses Health Study[S5+]	2007	United States	0	57.4	1,291	Prospective cohort study	No CHD	1.3	rs708272
Rotterdam[S33+]	2007	Netherlands	41	68.8	6,421	Prospective cohort study	Mixed Population	0.48	rs5882, rs1800775
British Womens' Heart and Health Study[S21++]	Unpblished	United Kingdom	0	68.9	3,570	Prospective cohort study	Mixed Population	2.58	rs708272
EPIC-Norfolk[S7++]	Unpublished	United Kingdom	63	65.3	2,114	Prospective cohort study	No CHD	2.2	rs1800775
Whitehall II[S3++]	Unpublished	United Kingdom	73	49.8	5,049	Prospective cohort study	Mixed Population	0.61	rs708272
ELSA [S2++]	Unpublished	United Kingdom	46	63.6	5,541	Prospective cohort study	Mixed Population	1.35	rs708272
Erasmus[S32 ++]	Unpublished	Netherlands	40.7	53.12	873	Prospective cohort study	Mixed Population	0.024	rs5882

Table S3. Traits included from studies evaluating *CETP* Taq1B and -629C>A genetic variant in European descent individuals ("0" for not included and "1" for included)

Study	HDL-C	LDL-C	Total Cholesterol	Triglycerides	HDL2	HDL3	ApoA1	ApoB	SBP	DBP	PP	Glucose	BMI	CRP	Electrolytes and renal measures	Use of antihypertensive medication	Smoking status	Use of Statin
REGRESS	1	1	1	1	0	0	0	0	1	1	0	0	1	0	0	1	1	1
Corella D	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rekyavik	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Brousseau	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0	0	0	0
Atherogene	1	1	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
CARE	1	1	1	1	0	0	0	0	1	1	0	0	1	0	0	0	0	0
PHS	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Marschang P	1	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
EARS	1	1	1	1	0	0	1	1	1	1	0	1	1	1	0	1	1	0
OPERA	1	1	1	1	0	0	0	0	1	1	0	0	1	0	1	0	0	0
Framingham	1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0	0
Arca M	1	1	1	1	0	0	0	0	1	1	0	0	0	0	1	0	0	0
ECTIM	1	1	1	1	0	0	1	1	1	1	0	0	1	0	0	1	1	0
NPHS II	1	1	1	1	0	0	1	1	1	1	1	1	1	1	0	0	1	0
WOSCOPS	1	1	1	1	0	0	1	1	1	1	0	1	1	1	1	1	1	1
ACCESS	1	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0
Sorli	1	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0
PREVEND	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1
SAPHIR	1	1	1	1	0	0	1	1	1	1	0	1	1	1	1	1	1	0
Busselton	1	1	1	1	0	0	0	0	1	1	0	0	1	0	0	0	0	0
CUDAS	1	1	1	1	0	0	0	0	1	1	0	1	1	1	0	0	0	1
CUPID	1	1	1	1	0	0	0	0	1	1	0	1	1	1	0	0	0	1
Intermountain	1	1	1	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1
Health Professionals Study	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nurses Health Study	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BWHHS	1	1	1	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1
EPIC	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	0
Rotterdam	1	0	1	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
Whitehall II	1	1	1	1	0	0	1	1	1	1	1	1	1	1	0	0	1	0
ELSA	1	1	1	1	0	0	0	0	1	1	1	1	0	1	0	1	1	0

Supplemental Figures and Figure Legends:

Figure S1 LD structure of the *CETP* gene. r^2 values are given from the ACCESS study. The main SNPs evaluated in this study were Taq1B (rs708272) and -629C>A (rs1800775) which are in LD (r^2=0.73). SNPs contributing to variance in HDL cholesterol identified from genome wide association scans are also shown (rs12596776, rs2217332, rs3764261, rs1800775, rs711752, rs1864163, rs7205804, s5880, rs5882, rs1800777, rs1566439). Data provided by J F Thompson, ACCESS study[16]

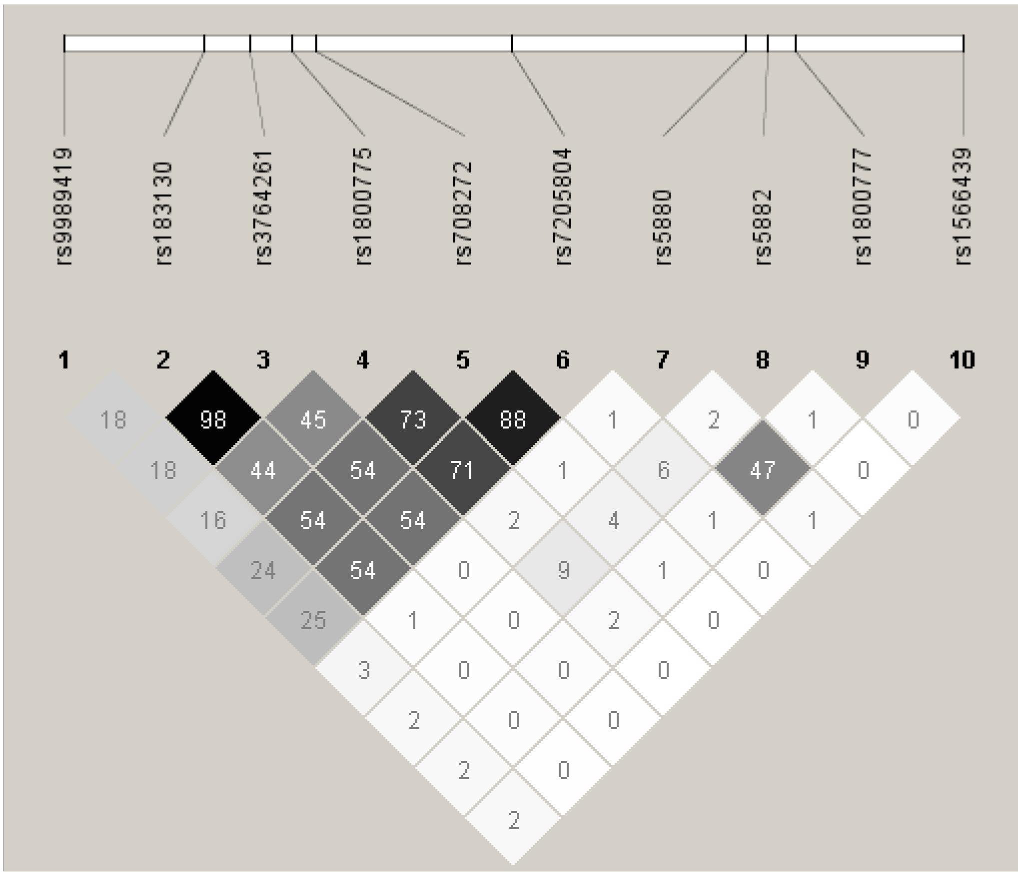
Figure S2a and S2b Standardised mean differences in lipid and lipoproteins between individuals homozygous for *CETP* variants in populations studies (a) and and those receiving torcetrpaib 60mg (b) daily as compared to placebo in clinical trials

Figures S3a-c Effect of *CETP* genotype on (a) CETP concentration, (b) CETP activity and (c) HDL cholesterol concentration. Forest plots indicate weighted mean difference and 95% confidence intervals. Results are stratified by ancestral origin, study size, and prevalent coronary heart disease, gender and polymorphism typed. (*the B1B1 genotype grouped is used as the reference group throughout)

Figure S4: Association between *CETP* genotype (B2B2 vs B1B1) and HDL-cholesterol level stratified by systolic blood pressure (SBP), diastolic blood pressure (DBP), pulse pressure (PP) and LDL-Cholesterol. Data from 6 studies, (12,983 individuals)

Figure S5a-b Effect of *CETP* genotype on (a) systolic and (b) diastolic blood pressure in populations of European descent only. Forest plots show weighted mean difference and 95% confidence intervals. Results are stratified by study size, prevalent coronary heart disease, gender, polymorphism typed, and strata of LDL cholesterol. (The B1B1 genotype is used as the reference group, see text for details)

Figure S1



rs9989419
rs183130
rs3764261
rs1800775
rs708272
rs7205804
rs5880
rs5882
rs1800777
rs1566439
1
2
3
4
5
6
7
8
9
10
18
98
45
73
88
1
2
1
0
18
44
54
71
1
6
47
0
16
54
54
2
4
1
1
24
54
0
9
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3
0
0
0
2
0
0
2
0
2

Figure S2a

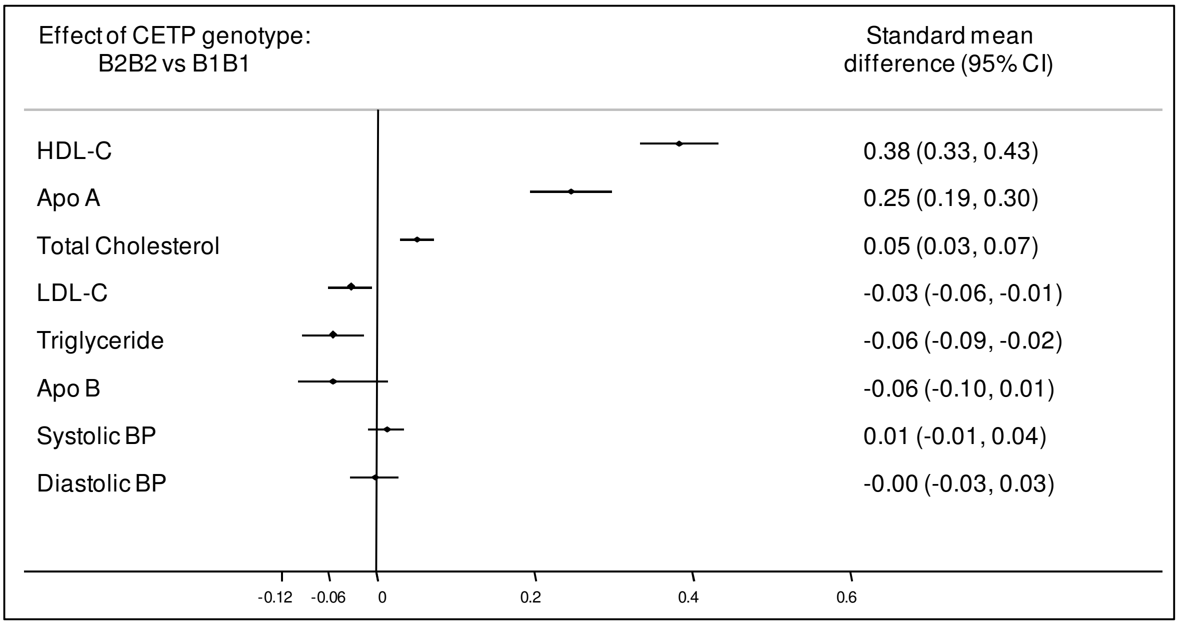


Figure S2b

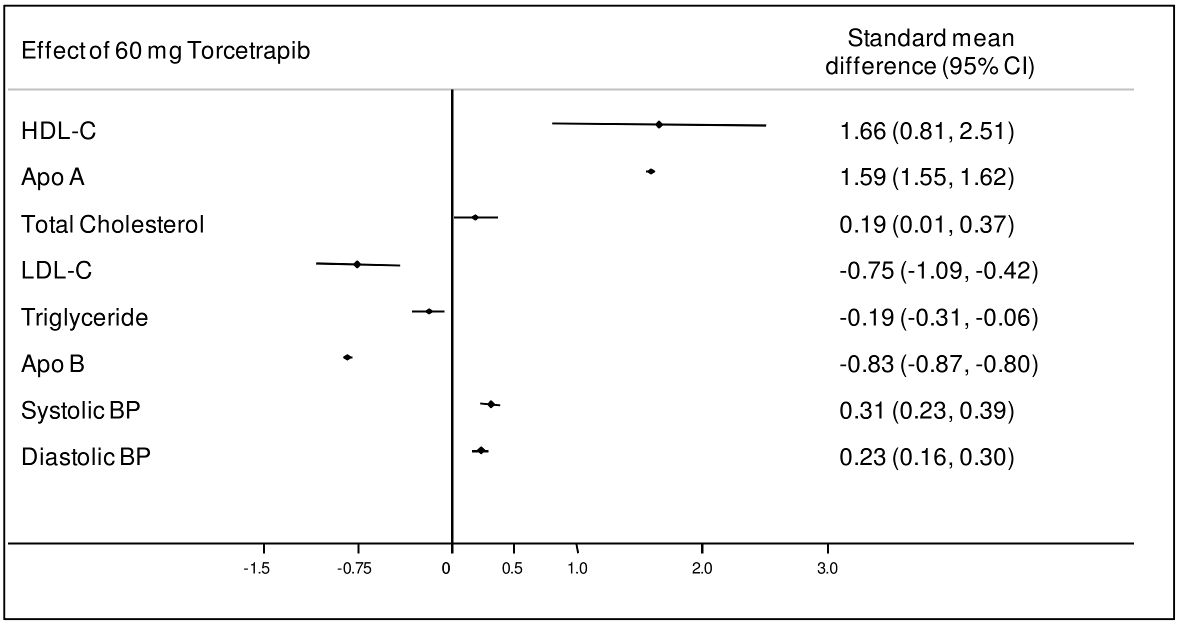


Figure S3a

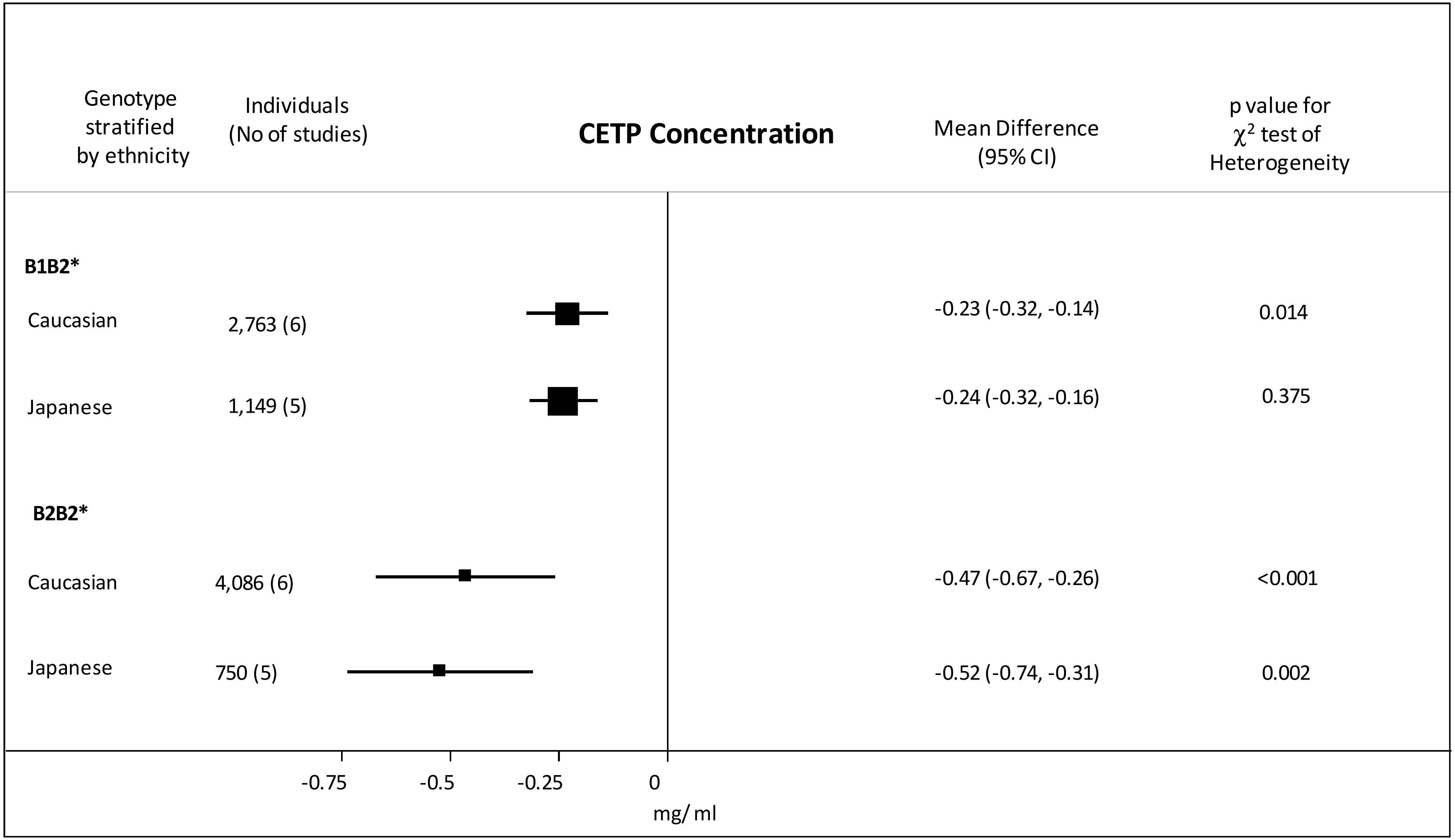

Genotype stratified by ethnicity
Individuals (No of studies)
CETP Concentration
Mean Difference (95% CI)
p value for χ2 test of Heterogeneity
B1B2*
Caucasian
2,763 (6)
-0.23 (-0.32, -0.14)
0.014
Japanese
1,149 (5)
-0.24 (-0.32, -0.16)
0.375
B2B2*
Caucasian
4,086 (6)
-0.47 (-0.67, -0.26)
<0.001
Japanese
750 (5)
-0.52 (-0.74, -0.31)
0.002
-0.75
-0.5
-0.25
0
mg/ ml

Figure S3b

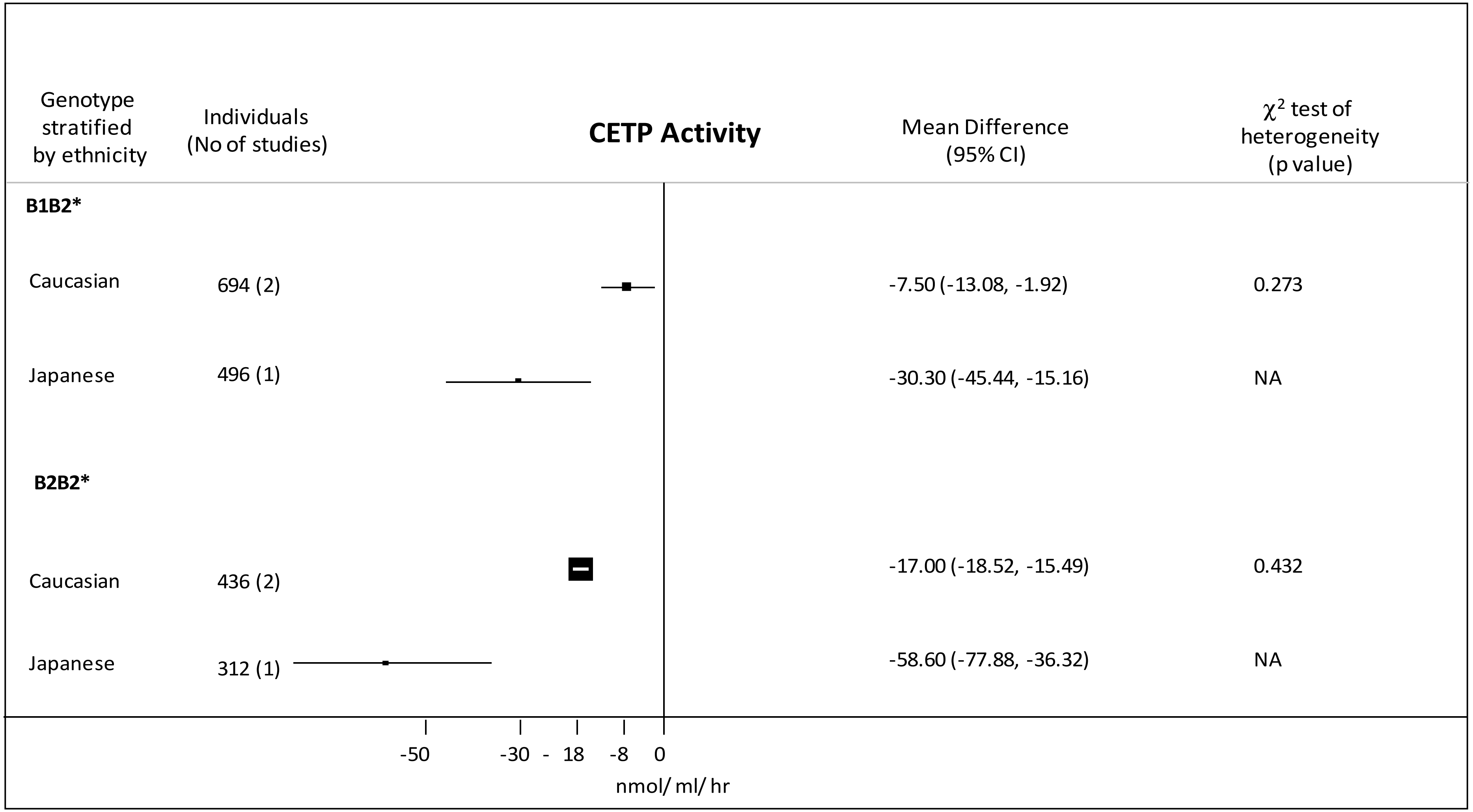
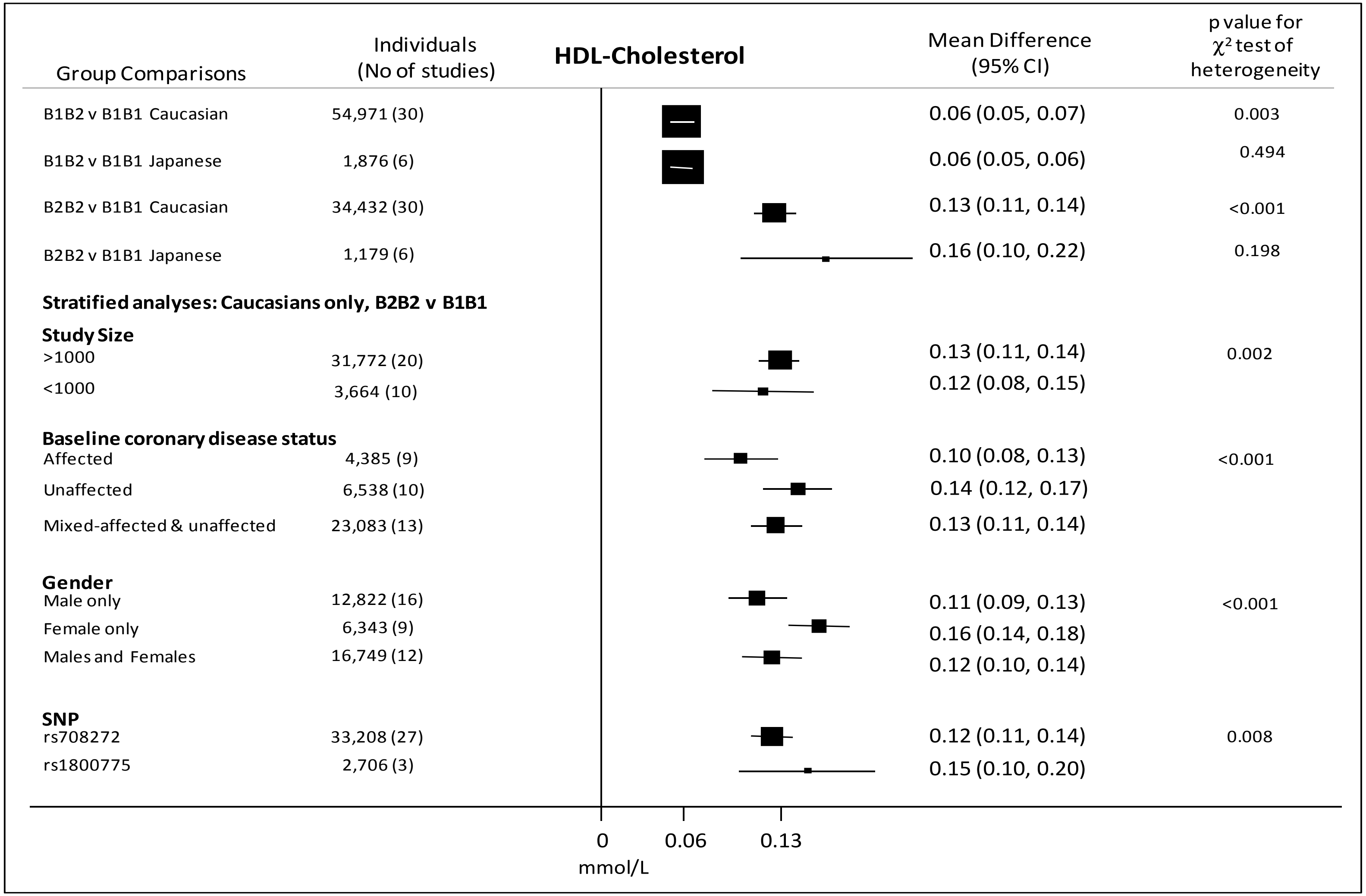
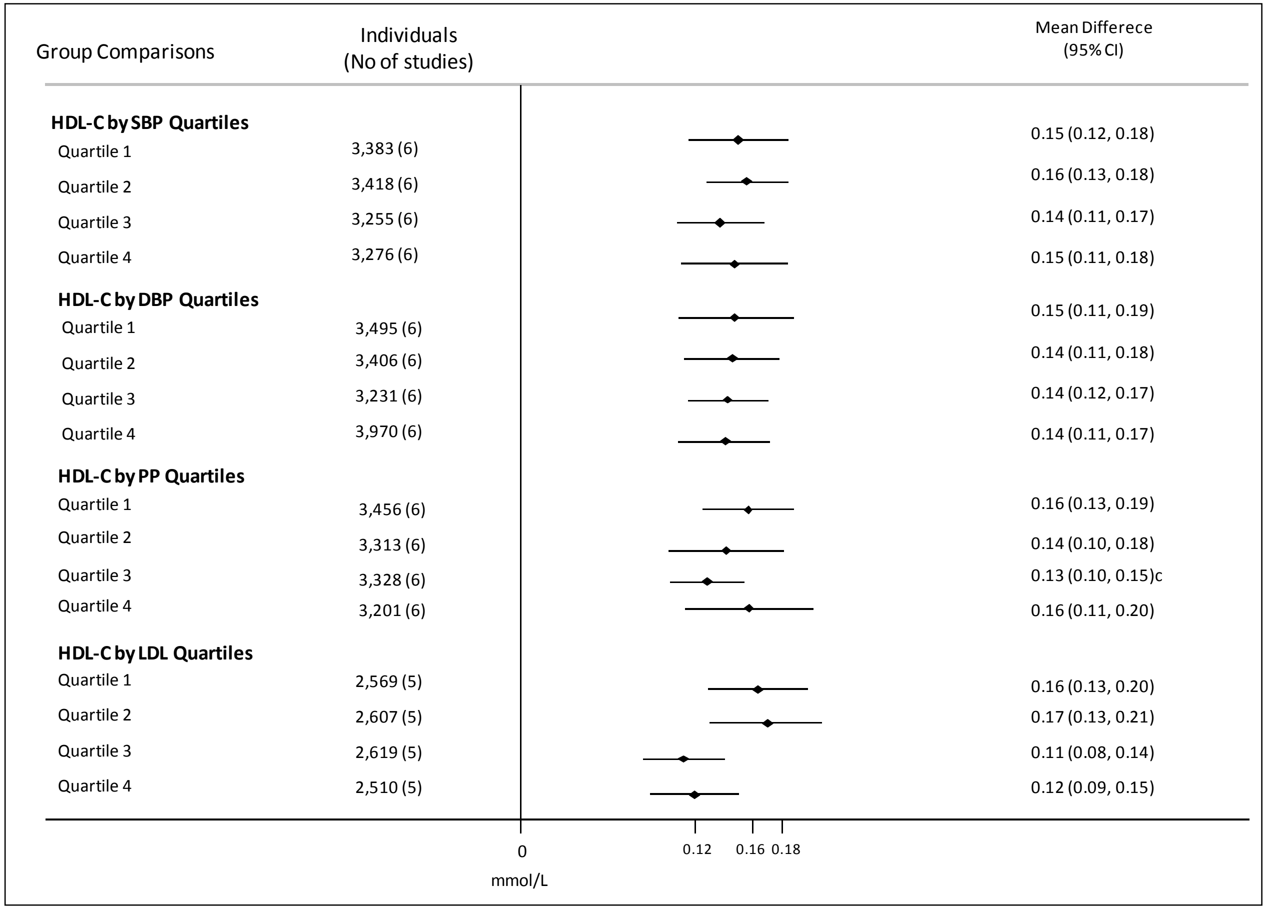

Genotype stratified by ethnicity
Individuals (No of studies)
CETP Activity
Mean Difference (95% CI)
χ2 test of heterogeneity (p value)
B1B2*
Caucasian
694 (2)
-7.50 (-13.08, -1.92)
0.273
Japanese
496 (1)
-30.30 (-45.44, -15.16)
NA
B2B2*
Caucasian
436 (2)
-17.00 (-18.52, -15.49)
0.432
Japanese
312 (1)
-58.60 (-77.88, -36.32)
NA
-50
-30
- 18
-8
0
nmol/ ml/ hr

Figure S3c



Group Comparisons
Individuals (No of studies)
HDL-Cholesterol
Mean Difference (95% CI)
p value for χ^2 test of heterogeneity
B1B2 v B1B1 Caucasian 54,971 (30) 0.06 (0.05, 0.07) 0.003
B1B2 v B1B1 Japanese 1,876 (6) 0.06 (0.05, 0.06) 0.494
B2B2 v B1B1 Caucasian 34,432 (30) 0.13 (0.11, 0.14) <0.001
B2B2 v B1B1 Japanese 1,179 (6) 0.16 (0.10, 0.22) 0.198
Stratified analyses: Caucasians only, B2B2 v B1B1
Study Size
>1000 31,772 (20) 0.13 (0.11, 0.14) 0.002
<1000 3,664 (10) 0.12 (0.08, 0.15)
Baseline coronary disease status
Affected 4,385 (9) 0.10 (0.08, 0.13) <0.001
Unaffected 6,538 (10) 0.14 (0.12, 0.17)
Mixed-affected & unaffected 23,083 (13) 0.13 (0.11, 0.14)
Gender
Male only 12,822 (16) 0.11 (0.09, 0.13) <0.001
Female only 6,343 (9) 0.16 (0.14, 0.18)
Males and Females 16,749 (12) 0.12 (0.10, 0.14)
SNP
rs708272 33,208 (27) 0.12 (0.11, 0.14) 0.008
rs1800775 2,706 (3) 0.15 (0.10, 0.20)
0
0.06
0.13
mmol/L

Figure S4



Group Comparisons
Individuals (No of studies)
Mean Differece (95% CI)
HDL-C by SBP Quartiles
Quartile 1
3,383 (6)
0.15 (0.12, 0.18)
Quartile 2
3,418 (6)
0.16 (0.13, 0.18)
Quartile 3
3,255 (6)
0.14 (0.11, 0.17)
Quartile 4
3,276 (6)
0.15 (0.11, 0.18)
HDL-C by DBP Quartiles
Quartile 1
3,495 (6)
0.15 (0.11, 0.19)
Quartile 2
3,406 (6)
0.14 (0.11, 0.18)
Quartile 3
3,231 (6)
0.14 (0.12, 0.17)
Quartile 4
3,970 (6)
0.14 (0.11, 0.17)
HDL-C by PP Quartiles
Quartile 1
3,456 (6)
0.16 (0.13, 0.19)
Quartile 2
3,313 (6)
0.14 (0.10, 0.18)
Quartile 3
3,328 (6)
0.13 (0.10, 0.15)c
Quartile 4
3,201 (6)
0.16 (0.11, 0.20)
HDL-C by LDL Quartiles
Quartile 1
2,569 (5)
0.16 (0.13, 0.20)
Quartile 2
2,607 (5)
0.17 (0.13, 0.21)
Quartile 3
2,619 (5)
0.11 (0.08, 0.14)
Quartile 4
2,510 (5)
0.12 (0.09, 0.15)
0
0.12
0.16
0.18
mmol/L

Figure S5a

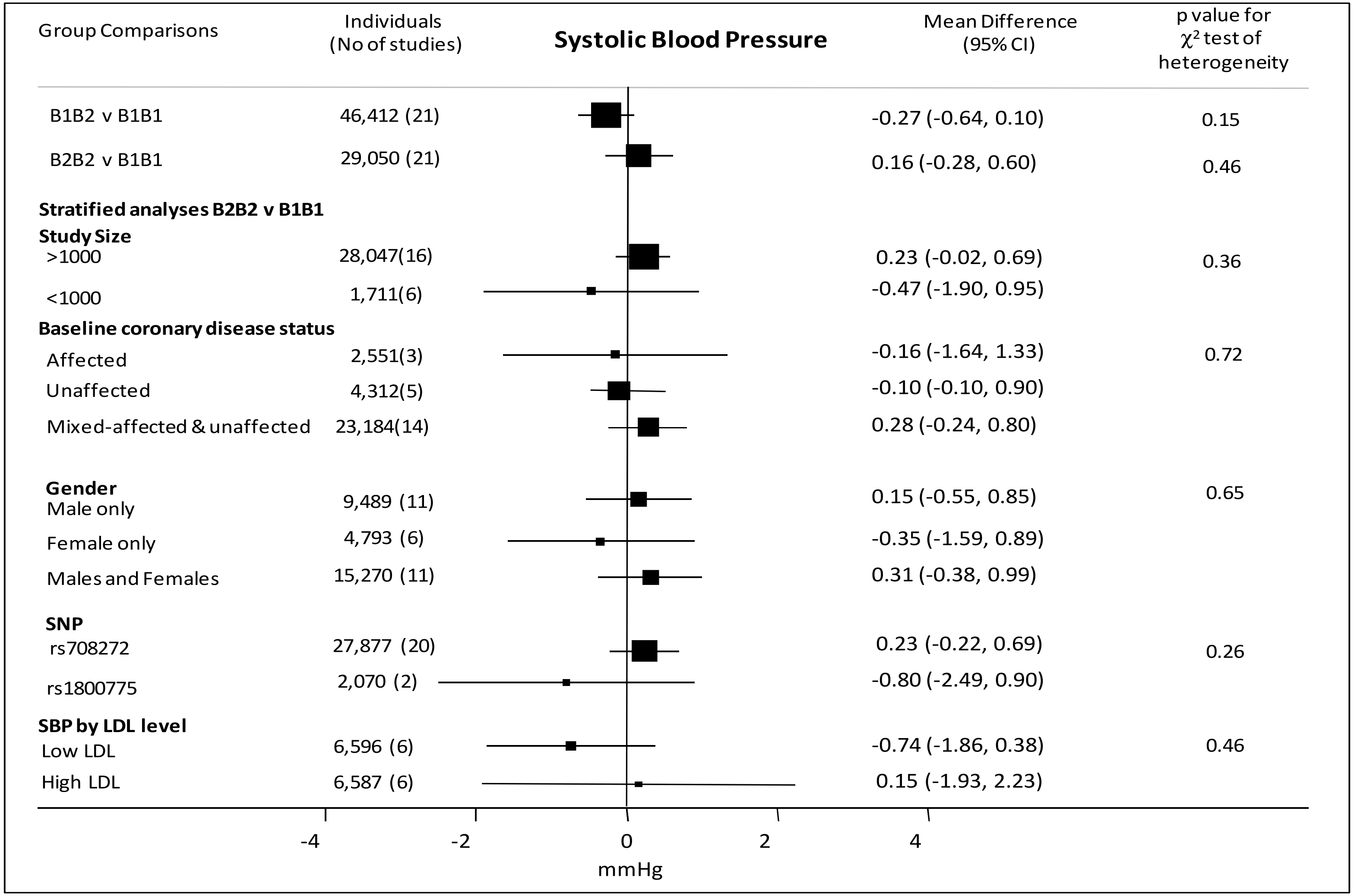
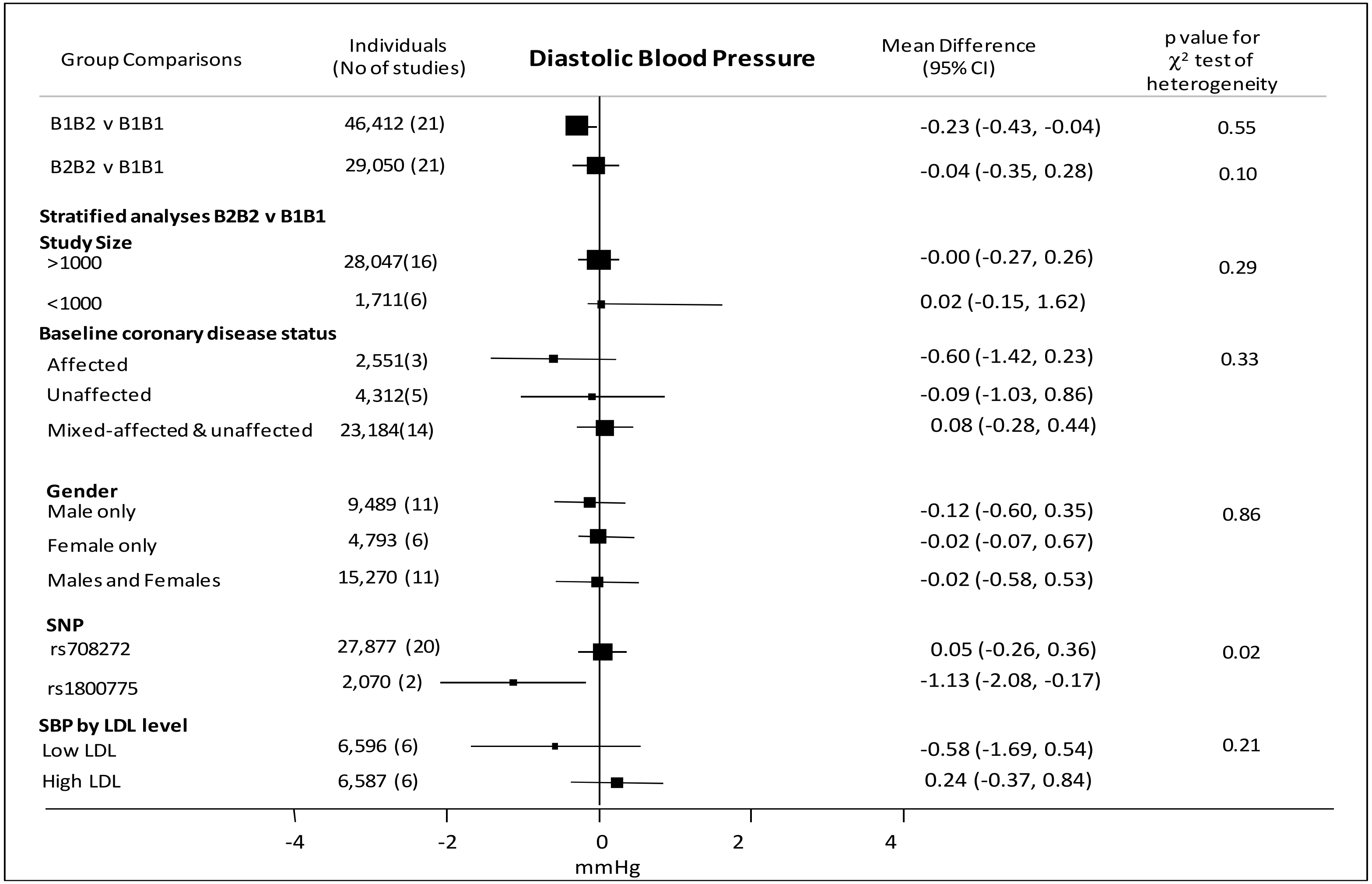

Group Comparisons
Individuals (No of studies)
Systolic Blood Pressure
Mean Difference (95% CI)
p value for χ^2 test of heterogeneity
B1B2 v B1B1 | 46,412 (21) | -0.27 (-0.64, 0.10) | 0.15
B2B2 v B1B1 | 29,050 (21) | 0.16 (-0.28, 0.60) | 0.46
Stratified analyses B2B2 v B1B1
Study Size
>1000 | 28,047(16) | 0.23 (-0.02, 0.69) | 0.36
<1000 | 1,711(6) | -0.47 (-1.90, 0.95)
Baseline coronary disease status
Affected | 2,551(3) | -0.16 (-1.64, 1.33) | 0.72
Unaffected | 4,312(5) | -0.10 (-0.10, 0.90)
Mixed-affected & unaffected | 23,184(14) | 0.28 (-0.24, 0.80)
Gender
Male only | 9,489 (11) | 0.15 (-0.55, 0.85) | 0.65
Female only | 4,793 (6) | -0.35 (-1.59, 0.89)
Males and Females | 15,270 (11) | 0.31 (-0.38, 0.99)
SNP
rs708272 | 27,877 (20) | 0.23 (-0.22, 0.69) | 0.26
rs1800775 | 2,070 (2) | -0.80 (-2.49, 0.90)
SBP by LDL level
Low LDL | 6,596 (6) | -0.74 (-1.86, 0.38) | 0.46
High LDL | 6,587 (6) | 0.15 (-1.93, 2.23)
-4
-2
0
2
4
mmHg

Figure S5b


Group Comparisons
Individuals (No of studies)
Diastolic Blood Pressure
Mean Difference (95% CI)
p value for χ^2 test of heterogeneity
B1B2 v B1B1 46,412 (21) -0.23 (-0.43, -0.04) 0.55
B2B2 v B1B1 29,050 (21) -0.04 (-0.35, 0.28) 0.10
Stratified analyses B2B2 v B1B1
Study Size
>1000 28,047(16) -0.00 (-0.27, 0.26) 0.29
<1000 1,711(6) 0.02 (-0.15, 1.62)
Baseline coronary disease status
Affected 2,551(3) -0.60 (-1.42, 0.23) 0.33
Unaffected 4,312(5) -0.09 (-1.03, 0.86)
Mixed-affected & unaffected 23,184(14) 0.08 (-0.28, 0.44)
Gender
Male only 9,489 (11) -0.12 (-0.60, 0.35) 0.86
Female only 4,793 (6) -0.02 (-0.07, 0.67)
Males and Females 15,270 (11) -0.02 (-0.58, 0.53)
SNP
rs708272 27,877 (20) 0.05 (-0.26, 0.36) 0.02
rs1800775 2,070 (2) -1.13 (-2.08, -0.17)
SBP by LDL level
Low LDL 6,596 (6) -0.58 (-1.69, 0.54) 0.21
High LDL 6,587 (6) 0.24 (-0.37, 0.84)
-4
-2
0
2
4
mmHg

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